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Title:
Perfect score:
Sequence:
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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AF009918 Streptoco BX005453 Danio rer AF009916 Streptoco Continuation (25 o Continuation (13 o Continuation (14 o AC116986 Dictyoste AY277504 Plasmodiu	טססס	BX5310939 Danio rer BX537105 Danio rer Continuation (4 of BX004991 Danio rer	09912 Strept 09911 Strept tinuation (4 29250 Zebraf 29469 Danio	3 4 5 7 6	AL935272 Danio rer AF009920 Streptoco Continuation (8 of AC007926 Trypanoso BX530070 Danio rer	M S S S S S S S S S S S S S S S S S S S	1 1 1 1	Description

## ALIGNMENTS

REFERENCE AUTHORS	SOURCE ORGANISM	VERSION KEYWORDS	ACCESSION	DEFINITION	LOCUS	AE006482	RESULT 1
Streptococcus.  1 (bases 1 to 11289)  1 (bases 1 to 11289)  Ferretti,J.J., McShan,W.M., Adjic,D., Savic,D., Savic,G., Lyon,K., Primeaux,C., Sezate,S.S., Surorov,A.N., Kenton,S., Lai,H., Lin,S.,	Streptococcus pyogenes M1 GAS Streptococcus pyogenes M1 GAS Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;	AE006482.1 GI:13621422	the complete genome. AE006482 AE004092	rain SF37	AE006482 11289 bp DNA linear BCT 01-JUN-2001		

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PUBMED
REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ferretti,J.J., McShan,W.M., Adjic,D., Savic,D., Savic,G., Lyon,K., Primeaux,C., Sezate,S.S., Surorov,A.N., Kenton,S., Lai,H., Lin,S., Qian,Y., Jia,H.G., Najar,F.Z., Ren,Q., Zhu,H., Song,L., White,J., Yuan,X., Clifton,S.W., Roe,B.A. and McLaughlin,R.E.
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complement(3121...3993)
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kinase(I) subunit"
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[Streptococcus pyogenes]"
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Submitted (03-APR-2002) Tohru Miyoshi-Akiyama, Tokyo Women's Submitted (03-APR-2002) Tohru Miyoshi-Akiyama, Tokyo Women's Medical University, Department of Microbiology and Immunology; Kawada-cho, Shinjuku-ku, Tokyo 162-8666, Japan (E-mail:KFA01112@nifty.ne.jp, Tel:81-3-3353-8111(ex.22713), Fax:81-3-5269-7411)
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Similarity AAAAACTCAAAACGATTTACTGTCACTTTAGTGGGAGTCTTTTTAATGATCTTCGCTTTG ATGAAAAAAACAAGGTTTCCAAATAAGCTTAATACTCTTAATACTCCAAAGGGTATTAAGT GAAAGTTTTAAAAGGGACTCAGAAAGTAACTTGGTTAGTACTTCTCAAATTATCTTTGATG AGAGTTACACAAGAGGCGGTATGGTACTATTCTGATAATGCTCCTATTTCTAATCCAGAT GCGATGAGCCCTAGAATTACGGGAGATGAGCTAAATCAGAAGTTACGAGCTGTTATGTAT 480 GCAATAAATCCAGATTCAAGTTCGGAATACAGATGGTATGGATATGAATCTTATGTAAGA GTAACTTCCATGGTTGGTGCTAAGACTGTTTTTGGTTTAGTAGAATCCTCGACGCCAAAC GTAACTTCCATGGTTGGTGCTAAGACTGTTTTTGGTTTAGTAGAATCCTCGACGCCAAAC AATGGACATCCACAAAATGCCAATGGTATTATGGAAGGCTTGGAACCCTTGAATGCTATC GCGATAAGCCCTAGAATTACGGGAGATGAGCTAAATCAGAAGTTACGAGCTGTTATGTAT AGTAGTGTTAAAAAGTGGTATAAAAAACATGATGGAATCTCTACAAAATTTGAAGATTAT GCAATAAATCCAGATTCAAGTTCGGAATACAGATGGTATGGATATGAATCTTATGTAAGA AATGGACATCCACAAAATGCCAATGGTATTATGGAAGGCTTGGAACCCTTGAATGCTATC AGTAGTGTTAAAAAGTGGTATAAAAAAACATGATGGAATCTCTACAAAATTTGAAGATTAT AGAGTTACACAAGAGGCGGTATGGTACTATTCTGATAATGCTCCTATTTCTAATCCAGAT Conservative 99.98; 0; Score 2270.8; Pred. No. 0; 0; Mismatches DB 1; 2 Indels Length 0; Gaps 153 600 540 573 513 420 453 360 393 300 240 180 60 753 660 693 633 333 273 213

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Bessen, D.E. and Kalia, A. Genomic localization of a T zone encoding extracellular
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Streptococcus pyogenes
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Bessen,D.E. and Kalia,A.
Direct Submission
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CDS

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o 9	Оу 8	Qy 7	Оу 7 Db 60	Qy 67 Db 599	Оу 6 Дъ 59	Qy 55 Db 587	Qy 49 Db 581	Qy 43 Db 575	Qy 37 Db 569	Qy 3 _Db 56	Qy 25 Db 557	Qy 1 Db 55	Qy 141 Db 5457	Qy Db 53	Ο <sub>γ</sub> 53	Query Match Best Local Matches 140		
15 ATTGCTTGAAGG		795 TTTGAGTGGTGGT	735 GCTAAGTATTTT             054 ACTGAATATTTT	<b>4</b> 0	615 GGAGTCAGAAAC	7	7	7	7	315 AGTITATIGCITTAAT 	7 5	195 TTCAAGTTCGGI	TC TA	81 TGTCACTTTAG7	21 AAATAAGCTTA              337 AAAATTGCAAA	Similarity 9; Conservat	GGTTT DSSGF ATKGI VVDTT	DTLTS
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TCTAA 6215 GCGAG 974 	914				TTGAA 674   TACTC 5993	AAAAG 614 TCTGA 5936	CAAGA 554       CAACA 5876	CCACA 494      CCTAA 5816	CCTAG 434       CCTAA 5756	AAAAA 374       AAACA 5696	TATCA 314       TACCA 5636	TATTA 254       TACTA 5576	AGA 194 	GGTGC 140        GGTGC 5456	TTTAC 80       TTAAC 5396	Gaps 10;	ELAGATMELR EQGQVTVNGK SDLIIGGQGE MYGDSGCKTE	WSFEEKNLKK
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1965 AACCATTAATTT             7290 TTCATTTAATCT		1845 7170	1788 7110	7 1					6756		6636 AGGAACTATAG	- O L	. o L		. 6	. o ⊢	975 6276	6216 ACTTCTAGAGGG
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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                      CDS
                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                     gene
                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7590 TGACTAAT 7597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LUBZ6 bp DNA linear BCT 19-DEC-Streptococcus pyogenes MsmR (msmR) gene, partial cds; LepA (lep Cpa (cpa), and Nra (nra) genes, complete cds; SsbA (ssbA) gene, partial cds; and unknown genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (19-FEB-1996) RWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Podbielski, A., Woischnik, M., Leonard, B.A.B. Characterization of nra, a global negative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U49397.1 GI:4028947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Microbiology,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Podbielski, A. and Woischnik, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              streptococc:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACATGACT 2272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTATTGCTTGTCCCATTTGGTTTGTTAGTGTTGTTTTGGTCGTAAAAGGACTAAAAAA 7589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GATAGTTATCGCTGGTATCAGTTTGGGGATCTGGGGAATTCACACGATAAGGATAAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCGTAAAGATCTTGTCCCACCAACTGGTTTTATTACTGATGGTGGAACCTATCTGTGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAATAAAGAGCCTGTTGTTCCTACAGGAGTTGATCAAAAGATCAATGGCTATCTAGCTTT 2204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCAAGAAGCTCAATCAGCAAGTGAGAATGTCACAGCAGACAAAGAAGTCACTTTTGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGCAAATGCTACAGTTTCAAAAACAGGAATAACAAGTGATGAGACACTTGCTTTTGAAAA 2144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 10826)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 10826)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Microbiol. 31 (1999) In press
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                                                                                                                                                                                                                                                                                                                                                                                                                                          location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                 function="multiple sugar metabolism regulator"
                                                                                                                                                                                                                                                                                                                                        . 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pauwelsstrasse
                                      . 1377)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aachen, Institute of Medical 30, Aachen, Nrw, Federal Rep
                                                                                                                                                                                                                                                                                                                                                                                                      pyogenes"
                                                                     terminator"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               regulator gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schmidt, K.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BCT 19-DEC-1998
s; LepA (lepA),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Republic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of.
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·10_signal
                                                                                                     -10_signal
                                                  35_signal
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KGKISTLLRVRGI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PSYTDDNVLMPKADYSFKVEADDNAKGKTKDGLDIKPGVIDGLENTKTIRYSNSDKI
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complement(5972.
                                                                                                   CHPDDLVDVIRMEDKKQEVIPVTHSLTVKKTVVGELGDKTKGFQFELELKDKTGQPIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(3705.
/gene="cpa"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to electron transfer flavorprotein 1 of Methylophilus electron; ORF 3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(3191. .3712)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(3191. .3712)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KFVAFSTCENFSTDNRVIVVGTIQE"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(1394.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="cpa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="LepA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="lepA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="collagen-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="lepA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .3169)
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S.C.D.S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="ORF 5;
8024. .8857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="extended 6297. .6302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="extended promoter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KPDLVITHSRLIPFVKNDLVKGVTVAEFSFDKPDYSIASIQNLIYQLKDKKYQDFLNE
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Beres, S.B., Sylva, G.L., Barbian, K.D., Lei, B., Hoff, J.S., Mammarella, N.D., Liu, M.-Y., Smoot, J.C., Porcella, S.F., Parkins, L.D., McCormick, J.K., Leung, D.Y.M., Schlievert, P.M.
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Beres, S.B., Sylva, G.L., Barbian, K.D., Lei, B., Hoff, J.S.,

Mammarella, N.D., Liu, M.-Y., Smoot, J.C., Porcella, S.F.,

Markins, L.D., McCormick, J.K., Leung, D.Y.M., Schlievert, P.M.
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Streptococcus pyogenes MGAS315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome sequence of a serotype M3 strain of group A Streptococcus: Phage-encoded toxins, the high-virulence phenotype, and clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Musser, J.M.
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AE014138 AE014074
AE014138.1 GI:21903795
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                                                                                                                                                                                         gordonii]
                                                                                                                                                                                                    putative ABC
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                                                                                                                                                                                                        /note="best non-GAS blastp hit: gb|AAC45310.1| (U81957)
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                                                                                                                                                                                                                                                                                                                                                                        /serotype="M3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2273. .2716
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(AE006440) hypothetical protein
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HFPAFFIGFCSGLILLEGMVMLRWRSOSRLKLYSRLSRYPFLGKLLKQYLTSYYAREW
GTLIGOGLDLMTILDIMAIEKSSLMKELAEDIRMSLLEGOAFHIKVATYPFFKKELSL
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ComYC (Streptococcus gordonii)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="comYB"
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                                                                                                                                               note="synonym: SpyM3_0083"
                                                                                                                                                                                                                                                                                                                                                                            codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SpyM3_0080"
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[Lactococcus lactis subs
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hypothetical protein [Streptococcus pyogenes M1 G
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kinase (Streptococcus pyogenes M1 GAS]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="best blastp hit: gb|AAK33225.
hypothetical protein [Streptococcus
/codon_start=1
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3368. .3694
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                                                                                                                                                                                                                                                                                                                                                      {	t NAPLMRQDVIGGLTWFGMDIDPEKNVFGYRGDISTPESKVKVLVISTDEELCIARDVE}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="ackA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="best non-GAS blastp hit: (AE006431) hypothetical protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="putative com
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[Lactococcus lactis subs
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901 GGTGATTACTCTAAATTGCTTGAAGGTGCAACATTACAGTTGACAGGGGATAACGTGAAT 960	721 CCGGATGATITITCAGCTAAGTATITITGAGTCTGAGGACAAGGGAGATAAATATAATAAA 780	541 AGACTTACACAAGAGGCGGTATGGTACTATTCTGATAATGCTCCTAATTCTAATCCAGAT 600	361 AGTAGTGTTAAAAACTGGTATAAAAACATGATGATCATCTACAAAATTTGAAGATTAT 420	5 % % %	Query Match  29.2%; Score 664.4; DB 1; Length 52900;  Best Local Similarity 60.0%; Pred. No. 2.1e-103;  Matches 1318; Conservative 0; Mismatches 816; Indels 64; Gaps 10;  4
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	. D		0 Db	Q D Q D Q Q	
1957 GGTAAAGCAACCATTAAATTAAACATTGGGAAAGTTTAACACTTCAAGGTTTACCAGAA 2016	OT GAAGATTAACTGCTATAACTGTTAAAACAGACTCTGGAGAACTAAAAGATTAAAAAACTGTT  AGCAGAACTAACTGCTATAACTCCTATTACTCACACAAGTTAAAACTGTT  ACTGGTTTAGCTGGTGACAGAACTAAAGATTTCCATTTTGAAATTAAAAAATAAT  ACTGGAACTATTGCAGAAAAAAAAAA		53 92 97 07 52 67	15 GATTGGTGGGAAAACATATCAAAAAAAGTAATTGAGAAGGGGTTACAAGGGGAAAAAGGACTCAT  11	1081 ACTITIAAGGTTGAAGCTGGCAAAGTGTATACTATTATTGATGAAAACAGATTGAA 1137

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MEDLINE
REFERENCE
AUTHORS
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AUTHORS
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AP005141
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Streptococcus pyogenes SSI-1 DNA,
AP005141 BA000034
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Streptococcus pyogenes SSI-1
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Large-Scale Genomic Rearrangement in Invasive Strains and New
Insights into Phage Evolution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nakagawa,I., Kurokawa,K., Yamashita,A., Nakata,M., Tomiyasu,Y., Okahashi,N., Kawabata,S., Yamazaki,K., Shiba,T., Yasunaga,T., Hayashi,H., Hattori,M. and Hamada,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genome project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Japan (E-mail:ken@gen-info.osaka-u.ac.jp,
URL:http://www.gen-info.osaka-u.ac.jp/, Tel:81-6-6879-8365,
Fax:81-6-6879-2047)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (01-MAY-2002) Ken Kurokawa, Osaka University, Genome Information Research Center; 3-1, Yamadaoka, Suita, Osaka 565-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone was isolated from a patient presenting with toxic shock
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1742. .2878
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identity 100 in 451 aa"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'gene="SPs0001"
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VRAFDDENVMREQGREDAFVDPVADIDTINLELILADLESINKRYARVEKMARTQKD
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3480. .4595
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5237. .8740
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4665. .5234
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                                                                                                                                                                                                                                                                                                          SLTLDRVVNAVKFYLQENDFEKTMQKFNG"
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identity 99 in 189 aa"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to GB:AAK33149.1 (AE006472) percent
identity 98 in 371 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3480. .4595
/gene="SPs0004".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3480.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="conserved hypothetical protein"
/protein_id="BAC63098.1"
/db_xref="G1:28810160"
/translation="MYQIGSEVEMKKPHACVIKETGKKANQWKVLRVGADIKIQCTNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="similar to GB:AAK33148.1 identity 100 in 65 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="SPs0003"
2953. .3150
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IESLKAIKSETVKIHFLSPVRPFTLTPGDEEESFIQLITPVRTN"
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/protein_id="BAC63097.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /evidence=not_experimental
/transl_table=11
/product="putative transcription-repair coupling factor"
                                                                                                                    /note="similar to GB:AAK33151.1
identity 99 in 1167 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LMTYSSEKAVKEAGRLREEGKEYVVQDGDIMEFRFNV"
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                                                        evidence=not_experimental
                                                                                           /codon_start=1
                                                                                                                                                                               'gene="SPs0006"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /evidence=not_experimental
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Query Match
Best Local S
Matches 1318
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                                                                                                                    1318;
                                               61 AAAAACTCAAAAACGATTTACTGTCACTTTAGTGGGAGTCTTTTTAATGATGATCTTCGCTTTG 120
                                                                                                                                         Similarity
                          AACAAACGACGACAAACGACGATCGGATTACTGAAAGTATTTTTGACGTTTGTAGCTCTG 111843
                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="SPs0009"
9529. .9654
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RFENYPVEVDVLSRFRSKKGAETLERVRKGQIDI I IGTHRLLSKDVVFSDLGLIVID
EEQRFGVKHKETLKELKTKVDVLTTATP I PRTLHMSMGI IRDLSVI ET PPTNRY PVQ
TYVLENNPGLVREA I I REMDRGGO I FYVYNKVDT I EKKVAELQELVPEAS I GFVHGQM
SEI QLENTLI DF I NGDYDVLVATT I I ETGVD I SNVNTTLF I ENADHMGLSTLYQLRGRV
GRSNRIAYAYLMYR PDKVLTEVSEKRLEGING COFFT I ALBUNDLS I RGANILGA
GRSNRIAYAYLMYR PDKVLTEVSEKRLEGING COFFT I ALBUNDLS I RGANILGA
GRSNRIAYAYLMYR PDKVLTEVSEKRLEGING COFFT I ALBUNDLS I RGANILGA
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QKNQTTVIVQVESQYAKERLEKSFQDVGFLELVSALQIVSRESQIVIGAISSGFYFA
DEKLALITEHERIYHKK KKRARRSHISNAERLKDYNELAVGDYVYHNVHGIGRFLGIE
TIQIQGIHRDYVTIQYQNSDRISLPIDQISSLSKYVSADGKEPKINKLNDGRFQXTKQ
KVARQVEDIADDLKLYAERSQQKGFSFSPDDDLQRAFDDDFAFYETEDQLRSIKEIK
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9161. .9532
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SSTNIKLNDHIEISFGNKLLTVRVIEIKDSTKKEDALKMYEIISETRITLNEEA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="SPs0007"
8878. .9174
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GVFINPASDLIFEASDFQRGIEQLEKALQTAQDDKKSYLEDVLAVSKNGFKHKDIRKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="mkkpsivQlnnHyikkenlkkkfeeeeesQkrnrfmGwilvsmmf
LfilpTynLvkSyvDfekQNQQVvkLkkeyneLskSTkkekQlaerLkDDnfvkKyar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="putative cell division protein (DivIC)"
/protein_id="BAC63103.1"
/db_xref="GI:28810165"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="conserved hypothetical protein"
/protein_id="BAC63102.1"
/db_xref="GI:28810164"
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/note="similar to GB:AAK33152.1 (AE006472) percent
identity 100 in 98 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDIYKRIREIQSREDYLNLQDELIDRFGEYPDQVAYLLEIALLKHYMDNAFAELVERK
NNQVIVRFEVTSLSYFLTQDYFEALSKTHLKAKISEHQGKIDIVFDVRHQKDYRILEE
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ETLQFLRNFKSQGVLIVSLSGLRTLLFNPDVFTKSQIQLTVGEDYDSDTLTKQLMTIG
                                                                                                                                                                                                     /product="hypothetical protein"
/protein_id="BAC63104.1"
/db_xref="gi:2810166"
/translation="MMMDNIVKKIEAFLAFSDKKLAELQQENQKVKEESQYIQKN"
                                                                                                                                                                                                                                                                                                                    /codon_start=1
/evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                      /note="unknown"
                                                                                                                                                                                                                                                                                                                                                                                         /gene="SPS0009"
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identity 100 in 123 aa"
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/db_xref="GI:28810163"
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Pred. No. 1.3e-103;
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                                                                                                                                                                               ACTITTAAGGTTGAAGCTGGCAAAGTGT---ATACTATTATTGATGGAAAACAGATTGAA 1137
                                                                                                                                                                                                                               GGGACTTACGTTTTAAGTGAGCTAAAACCTCCTCAAGGATATGGAGTTGCCACACCCATT
                                                                                                                                                                                                                                                                                                                         GGTTTTCAGGAGAAAATTTTTGATAGTAACAAGTCTGGAGAGAAAGTAGAGCTACCTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGTCAAGCTTTGAAGCAACTGATTGATCCGAATTTGGCAACTAAAATGCCAAAACAAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTAGTGACTCAAAATGCTATTTGGTACTATACTGATAGTTCCTATATTTCTGATACTAGT 112317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTAACTTCCATGGTTGGTGCTAAGACTGTTTTTGGTTTAGTAGAATCCTCGACGCCAAAC 180
TTTAGCGTTTTAAC---TACACAAAACTATGCAAAATTTATTATGCAAAAAATAAAAAT
                                             AACCAAAATAAGGAAATCGCAGAGCCATATTCTGTAACAGCTTTCAATGACTTTGAAGAG
                                                                                       AATCCCAATAAAGAGATAGTAGAGCCTTACTCAGTAGAAGCATATAATGATTTTGAAGAA 1197
                                                                                                                                     ACTTTCCAAAATCTTTTAAGTGCTGAGTATGTTCCGGATACTCCCCCAAAACCAGGAGA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGATACCAAAATCTTTTGAGTGGTGGTTTTAGTTCCTACAAACCCACCAACTCCAGGAGACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCGCAAATTATCAGTTAAGTATTTTTCAATCT------TCTGATAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCGGATGATTTTCAGCTAAGTATTTTTGAGTCTGAGGACAAGGGAGATAAATATAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGTAATGCGCTAAAAAGATTAATTAATCCAAAAGAGGTAGAAAGTTTACCGAATCAGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAGCTTTTCAACAAGAAGAAACAGATCTTAAATTAGATTCACAGCAACTACAACTAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAAAGTTTTAAAAGGGAGTCAGAAAGTAACTTGGTTAGTACTTCTCCAATTATCTTTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGAGTTACACAAGAGGCGGTATGGTACTATTCTGATAATGCTCCTATTTCTAATCCAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AATGGACATCCACAAAATGCCAATGGTATTATGGAAGGCTTGGAACCCTTGAATGCTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCAGATAAACCAAGAATAGAAGACGGACAGTTACAACAAAATATATTGAGGATTCTCTAT 112197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGCATCCATATTATAAACAGTTTAGAGTAGCACACGATTTAAGGGTTAACTTAGAAGGA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATAGGAATAGTAGGGTTTTCTATCAGAGCGTTCGGAGCTGAAGAACAATCAGTGCCAAA- 111902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----AGAGCCTCCGGCTAAAACTGAAAAAACATCAGTCATTATCAGAAAATATGCGGAA 112593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AATGGATATCCTAATGATCGTAATGGGATAATGAAAGGGATAGATCCTCTAAACGCTATT 112257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCGATGAGCCCTAGAATTACGGGAGATGAGCTAAATCAGAAGTTACGAGCTGTTATGTAT 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGTAGTGTTAAAAAGTGGTATAAAAAAACATGATGGAATCTCTACAAAATTTGAAGATTAT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGCTACCCAGACTATAGTCCGTTAAAGACTTACCATAATTTAAAAGTAAATTTAGATGGA 112017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCAATAAATCCAGATTCAAGTTCGGAATACAGATGGTATGGATATGAATCTTATGTAAGA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGTGTTAGATCACAATGGTATAAAAAACTTGAAGGAACTAATGAAAACTTTATCAAGTTA 112137
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/gene="spyM18_0122" /note="best blastp match gb AAC97155.1  (U49397) unknown		RESULT 7	
/gene="spyM18_0122" complement(14182395)	CDS	Db 113904 CTATCTTTGGTTGTTTACTTGTTCCATTTGGGTTAT 113941	
1 (QELLANMILEELEGRENKFULLI ILVSEUNGLEKIERKGESE EQVUONESLEQII HQVHGEYPTMYEDYKVSPKMKIDGNSLDEVQNPQDLATVLKMIDTKLKELHLL" COMDIEMENI (1418 2395)	gene		_
/ PO C C C C C C C C C C C C C C C C C C		Qy 2137 TTTGAAAATAATAAAGAGCCTGTTGTTCCTACAGGAGTTGATCAAAAGATCAAAGATCAATGGCTAT 2196	
(streprocous pyogenes) /codon_start=1 /transl_table=11 /product="hypothetical protein" /protein id="Aa196032 1"		Qy 2077 CAAGAAGTAGCAAATGCTACAGTTTCAAAAACAGGAATAACAAGTGATGAGACACTTGCT 2136	- 0
/yeire spynto_vizi complement(7571398) /gene="spyn18_0121" /note="best blastp match gb AAC97156.1  (U49397) unknown	CDS	Qy 2017 GGTTATTCTTACCTTGTCAAAGAAACAGATTCTGAAGGCTATAAGGTTAAAGTTAATAGC 2076 	п о
/LIGHBIACLOG="MINNIALOGLVANKELVANKELVANKKINDKOQVHYVTEVLCQSFQLL EARGFISVYWGKLASTLVSYASKSGLMSIDGELRTRKYDKDGQVHYVTEVLCQSFQLL ESRAQRAMRENNVTNDLVDLVLEEDTLPF" COMplement(7571398) /GOOG="ROWN"8 0131"	gene	Qy 1957 GGTAAAGCAACCATTAATTTAAAACATGGGGAAAGTTTAACACTTCAAGGTTTACCAGAA 2016 	- 0
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		Qy 1837 ACTGGTTTAGCTGGTGACAGAACTAAAGATTTCCATTTTGAAATTGAAATTAAAAAATAAT 1896	п о
	CDS	Qy 1780 GAAGATAAAAAAGAAGTTATACCTGTAACTCATAATTTAACATTGAGAAAAACGGTG 1836 	
/mol_ype- genomic DNA /strain-macAs8232" /db_xref="taxon:186103" 107502	gene	OY 1720 TATCAATCTCTTATTGGAACTCAGTGGCATCCAGAAGATTTAGTTGGTATG 1779 	
111420  11420  1142	FEATURES Source	QY 1660 CAAGATAGTAATCCTCCACAGCTAACTGACTTGATTTCTTTATTCCGAATAACAATAAA 1719	
Direct Submission  Direct Submission  Submitted (31-JAN-2002) Laboratory of Human Bacterial  Pathogenesis/Rocky Mountain Laboratories/NIAID/NIH, 903 S. 4th St.,	TITLE JOURNAL	Qy 1600 GGTTTTGGAGACATGAATGATAGTACTTTTAGCAGTTGCTAAAATCCTTGTAGAATACGCT 1659	- 0
<pre>Z (bases I to 11420) Z (bases I to 11420) Smoot,J.C., Barbian,K.D., Van Gompel,J.J., Smoot,L.M., Smoot,J.C., Barbian,K.D., Sturdevant,D.E., Ricklefs,S.M., Chaussee,M.S., Sylva,G.L., Sturdevant,D.E., Ricklefs,S.M., Porcella,S.F., Parkins,L.D., Beres,S.B., Campbell,D.S., Smith,T.M., Zhang,O. Kapury V Dalv, I A Veasy I George and Musser.I M</pre>	AUTHORS	Qy 1552 TTCACTGATAGTGCTGAATTAGATAAGGATAAACTA	- 0
Proc. Natl. Acad. Sci. U.S.A. 99 (7), 4668-4673 (2002) 21927593 11917108	JOURNAL MEDLINE PUBMED	QY 1492 GAGTATAGTGGTCTAACTGAGACACAATTGCGTGCGGCTACTCAGTTAGCAATATATTAT 1551	- 0
S.F., Parkins, L.I Kapur, V., Daly, or quence and compar treptococcus str	TITLE	QY 1432 TTCTTAAAACATATCAAAAAAGTAATTGAGAAGGGTTACAGGGAAAAAGGACAAGCTATT 1491	п о
<pre>streptococcus. 1 (bases 1 to 11420) Smoot, J.C., Barbian, K.D., Van Gompel, J.J., Smoot, L.M., Chaussee, M.S., Sylva, G.L., Sturdevant, D.E., Ricklefs, S.M.,</pre>	REFERENCE AUTHORS	OY 1372 ATTGCAGGTCGTGACCTCTTTAAATATACTGTGAAACCAAGAGATACCGATCCTGACACT 1431	
Streptococcus pyogenes MGAS8232 Streptococcus pyogenes MGAS8232 Bacterla, Firmicutes, Lactobacillales, Streptococcaceae,	SOURCE ORGANISM	OY 1315 GATGGTGGGAAAACAATGACTCCAGACTTTACAACAGGAGAAGTAAAATACACTCAT 1371	
AE009963 11420 bp DNA linear BCT 03-APR-2002 Streptococcus pyogenes strain MGAS8232, section 11 of 173 of the complete genome. AE009963 AE009949 AE009963.1 GI:19747394	LOCUS DEFINITION ACCESSION VERSION	ICTGATITTAATAACTATGGTAAGTTTTACTATGGAAAAAATACT \$TTGTCTATTGCTTTAATGCAGATCTAAAATCTCCACCAGACTCT 	
	AE000963		

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misc_feature
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                                                                                                                                                                                                                      GAEEQSTETKKTSVIIRKYAEGDYSKLLEGATLKLAQIEGSGFQEQSFESSTSGOKLQ
LSDGTYILTETKSPQGYEIAEPITFKYTAGKVFIKGKDGQFVENQNKEYAEPYSYTAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MDKIIKSIAQSGAFRAYYLDSTETVALAQEKHNTLSSSTVALGR
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LLDENDKVKVAGGFMYQYLPGASEEEIARYEKRLQEMPAISHLLASKNHYDALLEAIY
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                                  ASDYEVSVNGKNAPDGKATKASVKEDETITFENRKDLVPPTGLTTDGAIYLWLLLLVL
                                                             VPNSNKYQSLIGTQYHPESLVDIIRMEDKQAPIIPITHKLTISKTVTGTIADKKKEFN
FEIHLKSSDGQAISGTYPTNSGELTVTDGKATFTLKDGESLIVEGLPSGYSYEITETG
                                                                                                                                 EGKEIKYTHILGADLFSYANNPRASTNDELLSQVKKVLEKGYRDDSTTYANLTSVEFR
AATQLAIYYFTDSVDLDNLADYHGFGALTTEALNATKEIVAYAEDRANLPNISNLDFY
                                                                                                                                                                                                  NDFDDSGFINPKTFTPYGKFYYAKNANGTSQVVYCFNVDLHSPPDSLDKGETIDPDFN
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/protein_id="AAL96936.1"
/db_xref="GI:19747400"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5345.
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RYLIAMLYSKFGIVIYPLDHLDNQIIYRFLSQSATNLRTSPWLEEPFSFYNMLLALS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QTGLTAVQLKYYCKELDDFFGNNLDITIKKGKIICCFVKPVKEFYLHQLYDTSTILKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="N-terminal fragment of Nra"
/protein_id="AAL96935.1"
/db_xref="GI:19747399"
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complement(4262. .4915)
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/gene="nra.1"
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complement/7220
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LKGETIAVREFRGLAPHYLAGTAGAAKVRGAVSRAETLAEVEAIFETVR"
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DINMGCPVNKVVKNEAGAKWLRDPDKIYHIVKEVTSVLDIPLTVKMRTGWADSSLAVE
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[Streptococcus pyogenes]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="cbp"
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GLWVWLIGRKGLKND"
                                                                                                                                                                                                                                                                                              translation="MQKRDKTNYGSANNKRRQTTIGLLKVFLTFVALIGIVGFSIRAF"
                                                                                                                                                                                                                                                                                                                                                                                                                               transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="synonym: spyM18_0126"
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(Streptococcus pyogenes]"
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1034 TAACTGAATTGAATTCTCCAGCTGGTTATAGTATCGCAGAGCCAATCACTTTTAAGGTTG 1093
                                                                                                                                                                                                                5493
                                                                                   974
                                                                                                                                                                  914 AATTGCTTGAAGGTGCAACATTACAGTTGACAGGGGATAACGTGAATAGTTTTCAAGCGA 973
                                                                                                                                                                                                                                 854 CAAATCAACCTCAAACGACTTCAGTACTTATTAGAAAGTATGCTATAGGTGATTACTCTA 913
                                                                                                                                                                                                                                                                                                 863;
                                                                                                                                                                                                                                                                                                                       Similarity
                                     AGAGTTTTGAAAGTAGTACTTCAGGACAAAAATTGCAGTTGTCGGATGGTACATATATTT 5672
                                                                              GAGTGTTTAGCAGTAATGATATTGGAGAAAGAATTGAACTATCAGATGGAACTTATACTT 1033
                                                                                                                                                                                                              CTACTGAAACTAAAAAAACGTCAGTCATTATTAGAAAATATGCTGAAGGTGACTACTCTA 5552
                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="
9246. .
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8489. .9229
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VDGSVAMSGSLFLDTRNHNDFTDDYSLIYGHHMAGNAMFGEIPKFLKKDFFNKHNKAI
IETKERKKLTVTIFACLKTDAFDQLVFNPNAITNQDQQRQLVDYISKRSKQFKPVKLK
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/protein_id="AAL96939.1
/db_xref="GI:19747403"
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AKYIVSTEGGOSDKKPVLFKNFFDTTSLKVTKKVTGNTGEHQRSFSFTLLLTPNECFE
KGQVVNILQGGETKKVVIGEEYSFTLKDKESVTLSQLPVGIEYKVTEEDVTKDGYKTS
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/protein_id="AAL96938.1"
/db_xref="GI:19747402"
/translation="MKKNKLLLATAILATALGTASLNQNVKAETAGVIDGSTLVVKKT
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NTNVMSPALSAGDGILYYRLTDRYHINDVVVYEVDNTLKVGRIVAQAGDEVSFTQEGG
LLINGHPPEKEVPYLTYPHSSGPNFPYKVPTGTYFILNDYREERLDSRYYGALPINQI
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/protein_id="AAL96937.1"
/db_xref="GI:19747401"
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6912. .7433
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|Streptococcus pyogenes]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="spyM18_0130"
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                                          TTACCGAAACGGGTGCTTCAGATTATGAGGTAAGTGTTAATGGAAAAAATGCACCAGATG
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Mol. Microbiol. 10 (5), 1049-1055 (1993)
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/protein_id="AAA26964.1"
/protein_id="AAA26964.1"
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/note="repeat domain
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                                                                                                                                                                        /note="repeat domain 1" 1631. .2170
                                                                                                                                                                                                                                                                                                LMGGOSESVEFTKDTQTGMSGQTTPQIETEDTKEPEVLMGGQSESVEFTKDTQTGMSG
QTTPQVETEDTKEPEVLMGGQSESVEFTKDTQTGMSGQTTPQIETEDTKEPEVLMGGQ
                                                                                                                                                                                                                                                                                                                                          LDGQEVPEKPSIDLPIEVPRYEFNNKDQSPLAGESGETEYITEVYGNQQNPVDIDKKL
PNETGFSGNMVETEDTKEPEVLMGGQSESVEFTKDTQTGMSGQTTPQVETEDTKEPEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Streptococcus
/mol_type="genomic DNA"
/strain="JRS75"
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Location/Qualifiers
                                                                                                                                                                                                              /gene="prtF"
                                                                                                                                                                                                                                                          ATGDIENVLAFLGILILSVLSIFSLLKNKQSNKKV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       function="binds fibronectin"
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Score 215.8; I
Pred. No. 5.1e-
0; Mismatches
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                        ; DB 1;
.1e-27;
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                                          Length 2845;
    Indels
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    27;
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KEYWORDS
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ACCESSION
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Direct Submission
Submitted (31-JUL-1992)
Braunschweig, FRG
revised by [4]
                                                                                                       Streptococcus pyogenes
Streptococcus pyogenes
                                                                                                                                               S.pyogenes Sfb gene
X67947 S42389
X67947.1 GI:511149
                                                      Talay, S.R.
                                                                                Streptococcus.
                                                                                           Bacteria; Firmicutes; Lactobacillales;
                                                                                                                                 fibronectin-binding
                                                                                                                                                                                                                                                         ACCTGGTGAGACGTCAGAACATAATCCTAAAACTC 1274
                                                                                                                                                                                                                                                                                  TCCAGGAGACCCACCAATGCCTCCAAATCAACCTC 865
                                                                                                                                                                                                                                                                                                           --AAAATGAAGCTTACCAAAATCTTTTAAGTGCTGAATATGTACCTGATGATCCCCCTAA 1239
                                                                                                                                                                                                                                                                                                                            ATATAAAGGATACCAAAATCTTTTGAGTGGTGGTTTAGTTCCTACTAAACCACCAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                ATCTTTGATGCGTCAAGCTTTGAAGCAACTGATTGATCCGAATTTGGCAACTAAAATGCC
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                         Talay,
                          GBF,
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                          Mascheroder Weg
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TITLE
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Best Local
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On Jul 17, 19
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2 (bases 1 to 1030)
Talay,S.R., Valentin-Weigand,P.,
Chhatwal,G.S.
Fibronectin-binding protein of St
the binding domain involved in ac
epithelial cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (13-JUL-1994) S.R. Talay, GBF, Mascheroder Weg 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
TTATGTAAGAGGGCATCCATATTATAAACAGTTTAGAGTAGCACACGATTTAAGGGTTAA
                                                                                                                                                                                                                                                                                              GGTATTAAGTAAAAACTCAAAACGATTTACTGTCACTTTAGTGGGGAGTCTTTTTAATGAT
                                                                         TGTGCCTCATAGAGTTAGTCAAAATCCT-----GAGTTTCCCTTGGTATGGTTATGATTT
                                                                                                     GACGCCAAACGCAATAAATCCAGATTCAAGTTCGGAATACAGATGGTATGGATATGAATC
                                                                                                                                                                       TTTGGCATCCGCGGGTGCTATCGGTTTTGGTCAAGTAGCCTATGCTGCCGATGAGAAGAC
                                                                                                                                                                                                                  CTTCGCTTTGGTAACTTCCATGGTTGGTTGCTAAGACTGTTTTTGGTTTAGTAGAATCCTC
                                                                                                                                                                                                                                                                     GGCACACAAAAAAGAAAAAGGCGATTTGCTGTCACTTTAGTGGGAGTCTTTTTATGCT
                                                                                                                                                                                                                                                                                                                                                                        Conservative
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ALKKLIDFKLSEESLKRVPSTFRLNIFESDDKLYQLISLMRV
ALKKLIDFKLSEESLKRVPSTFRLNIFESDDKLYQLISLBPALPFLDGDE
KTPELDGIP I EEGPQRR NESLLEPTLPPWILDGOEVPBYSESLEPALPPLMPELDGOE
VPEVPSESLEPALPPLMPELDGOEVPBKPSVDLP I EDPRYEFNKDQSPLAGESGETE
VITEVYGNQQNPVDIDKLPNETGFSCMWYETEDTKEBGVLMGGOSESVEFTKOTQTG
MSGQTTPQVETEDTKEFGYLMGOESVEFTKDTQTGMSGFS
GGQSESVEFTKDTQTGMSGQTTPQVETEDTKEPGYLMGGOSESVEFTKDTQTGMSGFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ETVTIVEDTRPKLVFHFDNNEPKVEENREKPTKNITPILPATGDIENVLAFLGILILS
VLPIFSLLKKOTKO"
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Qvayaadektvphrvsqupefpwygydfykgfytryhulqlulugsktyqaycfulkr
fepkkegsyfpuwykewdgseetfykyaduprkduessrvidveleknilrvlyngyp
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124. .2040
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/product="fibronectin-binding
/protein_id="CAA48133.1"
/db_xref="GI:511150"
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/mol_type="genomic DNA"
/strain="DSM 2071"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                   Score 180.2; DB 1;
Pred. No. 5.9e-21;
0; Mismatches 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            477
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Kline, J.B., Xu,S., Bisno,A.L. and Collins,C.
Identification of a fibronectin-binding prot
pathogenic group G streptococci
Infect. Immun. 64 (6), 2122-2129 (1996)
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U31115
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                                                                                                                                                           Submitted (06-JUL-1995) James
University of Miami, 1600 NW |
Location/Qualifiers
                                                                                                                                                                                                   Direct Submission Submitted (06-JUL-
                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus sp. 'group
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                                                    /mol_type="genomic DNA"
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/db_xref="taxon:1320"
252. .1994
                  /gene="gfbA"
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Miami, FL 33136, USA
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                  CCTGAGAATTATAAGTTAAATCTTTTTTTTCAAAAGATAACTCGATTCAAAAT
                                                                                        CGTGATGCTCTTAGAAAATTAATATCACCAGATTTAGAAAAAACAGTCAAAAATCAGTTG
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RKLISPDLEKTYKNALENYKSDKIKFIVKOUSIONLLKTERYVQDNLOKFGEEPKEESPK
RKLISPDLEKTYVKNQLPENYKLMLFISKONSIONLLKTEYVQDNLOKFGEEPKEESPK
REPENKIPDLDGHEIPEVPQEPSDPVIPPYILDGEEVPEVPSESLEPALPPLMPELDGQ
EVPEKPSLDLPILVPRYENNKDQSPLAGESGETEYITEVPUTTEDYKELPVLNGE
GFSGNNYETEDYKEPVLMGGGSESVEFTKDTQTGNGGGTTPQVETEDYKEPGVLMGG
QSESVEFTKDTQTGMSGQTTPQVETEDTKEPGVLMGG
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/trans1_table=11
/product="group G streptococcal
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/db_xref="GI:950169"
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8.3e-19;
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23, Lund 2
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Microbiology 144 (Pt 1), 119-126 (1998)
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                       GACGCCAAACGCAATAAATCCAGATTCAAGTTCGGAATACAGATGGTATGGATATGAATC
                                                                                                                                                           GGTATTAAGTAAAAACTCAAAACGATTTACTGTCACTTTAGTGGGGGGTCTTTTTAATGAT
     TGAGCCGAATCGTATTA---
                                                                    TTTTGCATGCGCGGGTTCTATCGGTTTTGGTCAAGTAGCCTATGCTGCGGATGAGAAGAC
                                                                                                                                          GGCACACACAAAAAGAAAAGGCGATTTGCTGTCACTTTAGTGGGAGTCTTTTTTATGCT
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VPSESLEPALPPLMPELDGEVPEVPSESLEPALPPLMPELDGEEIPPVPSESLEPAL
PPLMPELDGQEVPEKPSIDLPIEVPRYEFNNKDQSPLAGESTDYITVPQNEVBAN
PPLMPELDGQEVPEKPSIDLPIEVPRYEFNNKDQSPLAGESTDYITVPQNETEE
DIDKKLPNETGETSGNAVETEETKEPGYLMGGQSESVEFTKDTQAGMSGQTTPQVETEE
TKEPGYLMGGQSESVEFTKDTQTGMSGQTAPQVETEDTKEPEVLMGGQSESVEFKKDT
QAGMSGQTAPQVETEDTKEPEVLMGGQSESVEFTKDTQTGSSGFSTYSIVEDTRFKL
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NEIMKGIDPLNAILVTQNAIWYYSDSAPINDINNFFTSEANDLNIPPQQLTLMREALR
KLISSDENLVKQVPSNFKLSIFESSDKSYQNLLSAEYVPDDPPKPGDTSEHNPKTPEL
                                                                                                                                                                                                                                                                                                                                 VFHFDNNEPKVEEHREKPTKNITPILPATGDIENVLAFLGILILSVLSIFSLLKNKQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="mflrgekmnnkiflnkeasflahtkrkrrfavtlvgvffmlfac
AGSIGFGQVAYAADEKTEPNRINSNPEFPWYGYDSYSGRLLRYHNLKVNGSKEYQAYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="fibronectin/fibrinogen binding
/protein_id="AAC38155.1"
/db_xref="GI:2271467"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Streptococcus pyogenes"
/mol_type="genomic DNA"
/strain="EF1949"
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1. .2801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /serotype="M15"
/db_xref="taxon:1314"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="prtF15"
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                                Submitted (23-JUN-1997) Medical Microbiology, Lund University, Solvegatan 23, Lund 22362, Sweden
                                                                    Direct Submission
                                                                                    2 (bases 1 to 321)
Katerov, V.E., Andree
                                                                                                                                                     of the binding region
Microbiology 144 (Pt
                                                                                                                                                                                        Katerov, V., Andreev, A., Schalen, C. and Totolian, A.A. Protein F, a fibronectin-binding protein of Streptococcus pyogenes, also binds human fibrinogen: isolation of the protein and mapping
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                  Location/Qualifiers
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                                                                                    Andreev, A.S.,
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                                                                                    Schalen, C. and Totolian, A.A.
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                                                                                 (bases 1 to 313)
Katerov, V. E., Andreev, A.S., Schalen, C. and Totolian, A.A.
Direct Submission
Submitted (23-JUN-1997) Medical Microbiology, Lund Unive Solvegatan 23, Lund 22362, Sweden
                                                                                                                                                                                               Katerov, V., Andreev, A., Schalen, C. and Totolian, A.A. Protein F, a fibronectin-binding protein of Streptococcus also binds human fibrinogen: isolation of the protein and of the binding fibrinogen:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product-"fibronectin binding protein F"
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                                                                       Location/Qualifiers
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<1. .>321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Streptococcus pyogenes"
/mol_type="genomic DNA"
/strain="M4 strain Umea"
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Pred. No. 1.3e-06;
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AUTHORS
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ORGANISM
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Best Local
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                                                                                                                                                                                                                                                                                                               Sasaki,Y.,
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197 CAAGTTCGGAATACAGATGGTATGGATATGAATCTTATGTAAGAGGGCATCCATATTATA
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Mycoplasma penetrans genomic
AP004172 BA000026
AP004171
                                                                                                                                                                                                                   Infectious Diseases, Department of Bacterial Pathogenesis and Infection Control; 4-7-1 Gakuen, Musashimurayama, Tokyo 208-0011, Japan (E-mail:yuko@nih.go.jp, Tel:81-42-561-0771,
                                                                                                                                                                                                                                                                                                                    Sasaki,Y.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                 The complete genomic sequence of Mycoplasma penetrans, intracellular bacterial pathogen in humans Nucleic Acids Res. 30 (23), 5293-5300 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycoplasma penetrans
Mycoplasma penetrans
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                            Submitted (18-SEP-2001) Yuko Sasaki, National Institute
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                                                                                                                                                                                                         Fax:81-42-563-3315)
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104. .1006
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                  /note="clinical isolate"
                                                                                                                                  ∕organism≖"Mycoplasma
                                                                                                                                                            1. .293650
                                                                                                                                                                               Location/Qualifiers
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/transl_table=11
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Pred. No. 6.6e-06;
0; Mismatches 102
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1447. .2
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1197. .1
                                                                                                                                                                                                                                                                             3598.
                                                                                                                                                                                                                                                                                                                                              /translation="mfvnenrvkstfkkeeiknykdfdesdrsehlnngrifevokir
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2480. .3340
/gene="MYPE4660"
/note="MYPE4630 paralog"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2480.
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IIEEITKHFNILINGYFRVFLLGTLFNNTKLENGIKNDFKYKKYKSLYWENIVSYIYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MPKNPFNDFKTIKNFKKRKTELNGEEKVKTDDLGLEIAWGYLKQ
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AILSRIFFHGIHLLVFTLLAVLSYKVLPLGSITNHELSTREDVVVSFVGILYGLMLLF
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AVHLLKIANKISKSNLCTDFvLEkRSFIFRFIKILIGDLNA"
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3598. .4521
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/transl_table=4
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translation="MLRKSKESKKVFKTIKMIKKNSVDFENTEVKNVDLTETWDLLEK"
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/gene="MYPE4720" /note="max /gene="MYPE4720"

/evidence=not\_experimental

transl\_table=4

/codon\_start=1 /note="paralog STINEAIAIANASEYGLQGSVFTKDLEEARTIAKYLDTGTVNINRGSSRGPDIFPFIG

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nlglakiiptilvgntivekpatggslvssolakyfdoanfiaovenlytgkgsbigd
yilenkriogatftgssdigfklasklpmkplylelggkdaaivtnnadvelaakeii
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/db_xref="GI:26433929"
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EGINQLIMAGIIAGGALAGLTVAIVFRYFFVKFSGEVHKTHDNHSHDDHIFNLSDIDN
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6048. .
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/standard_name="gap"
                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="MYPE4710"
7204. .8640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PKAAWLVIFLILSHRTIDGFVLGGTVAKMSTGADLNLGLFITFILHIFVEVLIVYYRQ
VQYGQKRWKALFYNFVTLLAIVPVMVIGAYINQYLAQVAWILPFVNVSGGSIIAFVGV
IELVPEFLHYKRMSSKDWYKLIICYSVGIVFALFILSFHTHEHVEEHAHDHDHETTTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VNKYLKGCAKA IEDTKEPDIEKNTAYQY AALRHYMY SKKEKYNEVFCVYEDALRFFTE
HLKQLFAESEGKEGKGLLPVNCLFTTDLHSVGQFLQEGNQIFFETCISIKNPLNDVVI
NEFLKDEDGLGFLNGKKLDY INKVAASSTIDAHHIDGKIDIIQINLDNRNEESFGYLY
                                                                                                                                                                                                           dehydrogenase"
                                                                                                                                                                                                                                                                                               /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VLKLIANPKQYLSSLNNFNIVNNFQPV"
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NKKLFVIYIVMHFHLNLLDTFFFDTETNQSEKNVSKYKNRIIKPLYKBHVLLSIYKFY
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AIISRIFFHGFYLILFAIVSLIVYKLYVFNSFSEEIVRRKMHVSIISAIYGLNFVLSG
                                                                                                                                                                                                                                       /product="NADP-dependent glyceraldehyde-3-phosphate
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                                                                                                                                                                               'protein_id="BAC44260.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGAGATACCGATCCTGACACTTTCTTAAAAACATATCAAAAAAGTAATTGAGAAGGGTTA 1469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCCAGCTGGTTATAGTATCGCAGAGCCAATCACTTTTAAGGTTGAAGCTGGCAAAGTGTA 1109
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TCCGAATAACAATAACAATCTCTTATTGGAACTCAGTGGCATCCAGAAGATTTAGT 1763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAGTGAAGATGATTCTGAAGAGCTTTATGATGAATCAGATGAAGATAGTG---AATCATA
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                                                     AGATGATGAAGAAACTGAAGACTATGAATCTGATGAAAATAATGAGGAATACTCTGA
                                                                                                                                                                   CGAATCAGAAGATTCAGAAGAAAACAGTGAAGATGATTCTGAAGAACTTTATGATGAGTC
                                                                                                                                                                                                                           AGACTATCATGGTTTTGGAGACATGAATGATAGTACTTTAGCAG-----TTGCTAAAAAT 1643
                                                                                                                                                                                                                                                                                    TTCAGAAGAATAGTAGATGAATCTTATGATGAAGAAGATGATCCTGAAGAAACTGAAGA
                                                                                                                                                                                                                                                                                                                                         TACTCAGTTAGCAATATTATTTCACTGATAGTGCTGAATTAGATAAGGATAAACTAAA 1589
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                                                                                                          CCTTGTAGAATACGCTCAAGATAGTAATCCTCCACAGCTAACTGACCTTGATTTCTTTAT 1703
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/protein_id="BAC44262.1"
/db_xref="GI:26453932"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="similar to CagA protein of Helicobacter
AJ269854, Expect=2.4e-01, Identities=40%"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1764 TGATATTATTCGTATGGAAGATAAAAAAGGAAGTTATACCTGTAACTCATAATTTAACATT 1823
                                                                                                                                                                                                                                                                                                           Center code: SC
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
Contact: zfish-pelp@sanger.ac.uk
Contact: zfish-pelp@sanger.ac.uk
                                                                                                                                                                      Assembly program: XGAPA; version 4.5 chemistry: Dye-terminator; 100% of reads Consensus quality: 144211 bases at least Consensus quality: 14460 bases at least Consensus quality: 144678 bases at least
                                                                                                         Insert size: 145065; sum-of-contigs
Insert size: 156629; 0.9% error; agarose-fp
Quality coverage: 8.29x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                  Center project name: zC266K22
                                                                                                                                                                                                                                                                                                                                                                                                                                           Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Apr 5, 2003 this sequence version replaced gi:28949357.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Actinopterygii; Neopterygii; Teleostei; Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 145265)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AL935272.11 GI:29568638
HTG; HTGS_PHASE1; HTGS_ACTIVEFIN;
Danio rerio (zebrafish)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL935272 145265 bp
Danio rerio clone CH211-266K22,
                                                                                       coverage: 7.97x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (27-MAY-2003) Wellcome Trust Sanger Institute,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Andrew, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unordered pieces.
NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGATGAGACACTTGCTTTTGAAAATAATAAAGA
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Q30
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BASE COUNT
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Best Local Similarity 43.3%;
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                                                                                                                                                                                                                                                                                        TACTTTAGCAGTTGCTAAAATCCTTGTAGAATACGCTCAAGATAGTAATCCTCCACAGCT 1682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                  TGTAACTCATAATTTAACATTGAGAAAAACGGTGACTGGTTTAGCTGGTGACAGAACTAA 1862
                                                                                                                        GTGGCATCCAGAAGATTTAGTTGATATTATTCGTATGGAAGATAAAAAAAGAAGTTATACC 1802
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fragment_chain:1"
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/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="CH211-266K22"
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97778: gap of 100 bp
101129: contig of 3351 bp in length
101229: gap of 100 bp
145265: contig of 44036 bp in length
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Search completed: August 19, 2003, 12:03:45 Job time: 8158 secs